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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/005,429

DATE: 12/14/2001
TIME: 11:11:19

Input Set : A:\241421.txt
Output Set: N:\CRF3\12142001\I005429.raw

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3 <110> APPLICANT: Sewalt, Vincent
4   Hastings, Craig
5   Meeley, Robert
6   Hantke, Sabine
7   Jung, Rudolf
8   Everard, John
9   Allen, Stephen
11 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS
OF PROTEINS
13 <130> FILE REFERENCE: 5718-119 (035718/241421)
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/005,429
C--> 15 <141> CURRENT FILING DATE: 2001-12-03
15 <150> PRIOR APPLICATION NUMBER: 60/250,703
16 <151> PRIOR FILING DATE: 2000-12-01
18 <160> NUMBER OF SEQ ID NOS: 25
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 797
24 <212> TYPE: DNA
25 <213> ORGANISM: Zea mays
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (187)..(573)
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34   tgattatttc taggaaacac atgcgggaat gagggcacca ttatccgcgt ccagtggtgc   120
36   cgctactccg ctcacctca gtcctcagtt cctcacctag cggtagcggt gcgcggggag   180
38   acgtag atg gcg gct tcg gag gcg gca gcg gcg gca aca ccg gtg   228
39   Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Thr Pro Val
40   1 5 10
42   acg ccg aca gag ggg acg gtg atc gcg atc cac agc ctg gag gag tgg   276
43   Thr Pro Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp
44   15 20 25 30
46   agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att   324
47   Ser Ile Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile
48   35 40 45
50   gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att   372
51   Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile
52   50 55 60
54   ttt gct gat gat gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt   420
55   Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val
56   65 70 75
58   gat gtg gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc   468
59   Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala
60   80 85 90
62   atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc   516
63   Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val
64   95 100 105 110

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66 gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg      564
67 Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
68          115          120          125
70 gcc tgc tag atcagtgatg ccgtaatgta gtattcgctt aaataagagg      613
71 Ala Ser
74 acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggttaattcg tatgagagag      673
76 tgcccccttt ggtggtactt cttcgtatgt agtattaact cctgtcttaa tatgttgccc      733
78 tgcctgtgct tttcatacca tgtttgctct ttcagctgag gtgttaaaaa aaaaaaaaaa      793
80 aaaa      797
83 <210> SEQ ID NO: 2
84 <211> LENGTH: 128
85 <212> TYPE: PRT
86 <213> ORGANISM: Zea mays
88 <400> SEQUENCE: 2
90 Met Ala Ala Ser Glu Ala Ala Ala Ala Thr Pro Val Thr Pro
91 1          5          10          15
94 Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
95          20          25          30
98 Glu Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
99          35          40          45
102 Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala
103          50          55          60
106 Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val
107 65          70          75          80
110 Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro
111          85          90          95
114 Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly
115          100          105          110
118 Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met Ala Ser
119          115          120          125
122 <210> SEQ ID NO: 3
123 <211> LENGTH: 799
124 <212> TYPE: DNA
125 <213> ORGANISM: Zea mays
127 <220> FEATURE:
128 <221> NAME/KEY: CDS
129 <222> LOCATION: (69)..(455)
131 <400> SEQUENCE: 3
132 gtccgcgtcc agtgtgtccg ctccccctca gtccctcaact agcggtagcg tgcgcgcggg      60
134 agacgtag atg gcg gct tgc gag gcg gcg gcg gcg gcg aca cgg gtg      110
135          Met Ala Ala Ser Glu Ala Ala Ala Ala Thr Pro Val
136          1          5          10
138 gcg cgc aca gag ggg acg gtg atc gcg atc cac agc ctg gag gag tgg      158
139 Ala Pro Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp
140 15          20          25          30
142 agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att      206
143 Ser Ile Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile
144          35          40          45
146 gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att      254

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147 Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile
148                               50                               55                               60
150 ttt gct gat atg gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt      302
151 Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val
152                               65                               70                               75
154 gat gtc gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc      350
155 Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala
156                               80                               85                               90
158 atg oca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc      398
159 Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val
160 95                               100                               105                               110
162 gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg      446
163 Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
164                               115                               120                               125
166 gcc tcg tag atcagtgatg cegtaatgta gtattcgcc taaataagagg      495
167 Ala Ser
170 acgctctgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag      555
172 tgcccccttt ggtgtaact ctctgtatgt agtattaaact cctgtcttaa tatgttgccc      615
174 tgccttgctct ttcaatacca tgtttgctct ttcagctgag gtgttatatc gtaaatcgga      675
176 gtcaatatct ttgaatttga ttaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      735
178 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      795
180 aaaa
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 128
185 <212> TYPE: PRT
186 <213> ORGANISM: Zea mays
188 <400> SEQUENCE: 4
190 Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Thr Pro Val Ala Pro
191 1                               5                               10                               15
194 Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
195                               20                               25                               30
198 Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
199                               35                               40                               45
202 Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala
203                               50                               55                               60
206 Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val
207 65                               70                               75                               80
210 Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro
211                               85                               90                               95
214 Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly
215                               100                               105                               110
218 Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met Ala Ser
219                               115                               120                               125
222 <210> SEQ ID NO: 5
223 <211> LENGTH: 367
224 <212> TYPE: DNA
225 <213> ORGANISM: Zea mays
227 <220> FEATURE:
228 <221> NAME/KEY: CDS

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229 <222> LOCATION: (3)..(194)
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232 cc cgc ttc tcc gac gcc atc ttc gtc aag gtc gac gtc gac gag ctc      47
233   Arg Phe Ser Asp Ala Ile Phe Val Lys Val Asp Val Asp Glu Leu
234     1           5           10           15
236 gcg gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gta      95
237 Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val
238           20           25           30
240 ctt gtc aag gat ggg aag gag gta agc cgt gtg gtt ggg gcc aag aag      143
241 Leu Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys
242           35           40           45
244 gac gag ctt gag agg aag atc cgg atg ttc acg tca tct tcc tca tgc      191
245 Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser Ser
246           50           55           60
248 taa actcctgtgg ttgcctggg acggagttgc tgaagtgaat tggtcccttc      244
250 tctcaatgct gaaaaaagg gaaaaaacta tgtgaaaatg atggtagacg tgtctgggctc      304
252 agtaataaga gtttctaaaa tctgaatgag attggaatcg ctttcggtg ctgaaaaaaa      364
254 aaa                                                                    367

257 <210> SEQ ID NO: 6
258 <211> LENGTH: 63
259 <212> TYPE: PRT
260 <213> ORGANISM: Zea mays
262 <400> SEQUENCE: 6
264 Arg Phe Ser Asp Ala Ile Phe Val Lys Val Asp Val Asp Glu Leu Ala
265 1           5           10           15
268 Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
269           20           25           30
272 Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys Asp
273           35           40           45
276 Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser Ser
277           50           55           60

280 <210> SEQ ID NO: 7
281 <211> LENGTH: 720
282 <212> TYPE: DNA
283 <213> ORGANISM: Zea mays
285 <220> FEATURE:
286 <221> NAME/KEY: CDS
287 <222> LOCATION: (38)..(442)
289 <400> SEQUENCE: 7
290 aggcagcgag tgcaaacac cgcgagagcg atcagcg atg ggc tcc ttc ttc tgc      55
291           Met Gly Ser Phe Phe Ser
292           1           5
294 acc tta gtg acg ccc cct ccg ccc gcc gcc gac gac ccg aac tgc gcc      103
295 Thr Leu Val Thr Pro Pro Pro Pro Ala Ala Asp Asp Pro Asn Cys Ala
296           10           15           20
298 gtg gtg gcc gcg cac tcc aag gcc acc tac gac gag cag tgg gcg gcc      151
299 Val Val Ala Ala His Ser Lys Ala Thr Tyr Asp Glu Gln Trp Ala Ala
300           25           30           35
302 cac aag agc agc agc aag ctg atg gtg atc gac ttc tgc gcg tcc tgg      199

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303 His Lys Ser Ser Ser Lys Leu Met Val Ile Asp Phe Ser Ala Ser Trp
304 40 45 50
306 tgc ggg ccc tgc cgc ttc atc gag ccg gcc ttc aag gag ctg gcc tcc 247
307 Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala Phe Lys Glu Leu Ala Ser
308 55 60 65 70
310 cgc ttc acc gat gcc atc ttc atc aag gtc gac gtc gac gag ctc gcg 295
311 Arg Phe Thr Asp Ala Ile Phe Ile Lys Val Asp Val Asp Glu Leu Ala
312 75 80 85
314 gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gtg ctg 343
315 Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
316 90 95 100
318 gtc aag gat ggg aag gag gta gcc cgt gtg att ggg gct aag aag gac 391
319 Val Lys Asp Gly Lys Glu Val Gly Arg Val Ile Gly Ala Lys Lys Asp
320 105 110 115
322 gag ctt gag agg aag atc agg atg ttc gtc acg tca tct tcc tcg tcc 439
323 Glu Leu Glu Arg Lys Ile Arg Met Phe Val Thr Ser Ser Ser Ser
324 120 125 130
326 taa cttagcagtg catacaactcc cacettatta ctggtttctc gactccagtg 492
328 gttcgcttg gacgggggtg ctgaaatggt tcccttctct gaatactgaa aaatcaaaaa 552
330 aagaagtata tgaaaaaatg atggtagacg tgtctggggtc aataagagtt tctgaaactt 612
332 ggatttgtat gtgtcagttct ctgtgttctg ttccaagga atggatcatg tgagtttgga 672
334 atatagctgg aaatatgttg tgctgtttaa aaaaaaaaaa aaaaaaaa 720
337 <210> SEQ ID NO: 8
338 <211> LENGTH: 134
339 <212> TYPE: PRT
340 <213> ORGANISM: Zea mays
342 <400> SEQUENCE: 8
344 Met Gly Ser Phe Phe Ser Thr Leu Val Thr Pro Pro Pro Pro Ala Ala
345 1 5 10 15
348 Asp Asp Pro Asn Cys Ala Val Val Ala Ala His Ser Lys Ala Thr Tyr
349 20 25 30
352 Asp Glu Gln Trp Ala Ala His Lys Ser Ser Ser Lys Leu Met Val Ile
353 35 40 45
356 Asp Phe Ser Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala
357 50 55 60
360 Phe Lys Glu Leu Ala Ser Arg Phe Thr Asp Ala Ile Phe Ile Lys Val
361 65 70 75 80
364 Asp Val Asp Glu Leu Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala
365 85 90 95
368 Met Pro Thr Phe Val Leu Val Lys Asp Gly Lys Glu Val Gly Arg Val
369 100 105 110
372 Ile Gly Ala Lys Lys Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Val
373 115 120 125
376 Thr Ser Ser Ser Ser Ser
377 130
380 <210> SEQ ID NO: 9
381 <211> LENGTH: 722
382 <212> TYPE: DNA
383 <213> ORGANISM: Zea mays

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VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:775 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:777 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:783 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:787 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:789 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:791 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:846 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18